SEQUENCE LISTING

<110> Hilton, Douglas J.
      Willson, Tracy
      Nicola, Nicos A.
      Gainsford, Timothy
      Alexander, Warren S.
      Metcalf, Donald
      Ng, Ashley

<120> A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
      ENCODING SAME

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<140> 09/043,816
<141> 1998-09-17

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<170> PatentIn Ver. 2.0

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aactataagg tccatctttt atatgttctg cctgaagtgt tagaagattc acctctggtt 780

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4

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tgtgaaactg atgggtactt aactaaaatg acttgcagat ggtcaaccag tacaatccag 1620

tcacttgcgg aaagcacttt gcaattgagg tatcatagga gcagccttta ctgttctgat 1680

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tatgaatgca ttttccagcc aatcttccta ttatctggct acacaatgtg gattaggatc 1800

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ttaagtggaa aagaagtaca atggaagatg tatgaggttt atgatccaaa accaaaatct 2040

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aaggagaaaa atgtcacttt actttggaag cccctgatga aaaatgactc attgtgcagt 2280

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gtttcctgga tactatcacc cagtgattac aagctaatgt attttattat tgagtggaaa 2580

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ttgcttggaa cattattaat atcacaccaa agaatgaaaa agctattttg ggaagatgtt 2880

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atagagtatt agaagatttt tacattttga agaaggggag caaatctaaa aaaaattcag 3060

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5

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agtattttgt aattctttta ataccgacaa cgacagtaat gtatagataa tttacagtag 3300

tttatacatc atctgttagg acattaatcc acttgagatt ttgacgttgt agactgttta 3360

tcgaaatttt tatgttacta atattcatac cttagtcact tttataaatc aaacataaaa 3420

atacaggttt gaaaaggtaa aatctaagga aatatctgtg cagtcggatt tttagtcgga 3480

taagcccaca agaaaactta tagaggaccg taaaaacata gattgaaaca agttagaccc 3540

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ccttcgggct tcaacacaaa cacgacgggt gtcctgtcac cctcaatgtc aagtatagtc 3660

ctactgggat gtatgggtcc agtctaactg ccctggtctt cccttgtagc tgaagattac 3720

aggtgcgaaa gaacaaatta atactggatt tagattaaat gaaggtgact tggtaggttc 3780

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<222> (687)
<223> Xaa is unknown or other.

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Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
            20                  25                  30

Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Thr Asn Tyr Phe Leu
        35                  40                  45

Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
    50                  55                  60
```

6

Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
65   70   75   80

Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
            85   90   95

Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Arg Thr Phe Val
        100   105   110

Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
        115   120   125

Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
    130   135   140

Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
145   150   155   160

Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
            165   170   175

Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
            180   185   190

Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
        195   200   205

Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Xaa Ser
    210   215   220

Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
225   230   235   240

Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
            245   250   255

Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys
            260   265   270

Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
    275   280   285

Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
    290   295   300

Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
305   310   315   320

Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
            325   330   335

Pro Pro Lys Ile Leu Thr Ser Val Gly Ser Asn Val Ser Phe His Cys
            340   345   350

Ile Tyr Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp
        355   360   365

7

Trp His Asn Leu Ala Glu Leu Ile Pro Gln Ser Gln Tyr Asp Val Val
    370   375   380

Ser Asp His Val Ser Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys
385   390   395   400

Pro Arg Gly Leu Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His
            405   410   415

Gly Cys His His Arg Tyr Ala Gly Leu Tyr Val Ile Asn Val Asn Ile
            420   425   430

Asn Ile Ser Cys Gln Thr Asn Gly Tyr Leu Thr Lys Met Thr Cys Arg
        435   440   445

Trp Ser Thr Ser Thr Ile Gln Ser Leu Ala Glu Ser Thr Leu Glu Leu
    450   455   460

Arg Tyr His Arg Ser Ser Leu Tyr Cys Ser Asn Ile Pro Ser Ile His
465   470   475   480

Pro Ile Ser Glu Pro Lys Asn Cys Tyr Leu Gln Ser Asn Gly Phe Tyr
            485   490   495

Gln Cys Ile Pro Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp
        500   505   510

Ile Arg Ile Asn His Ser Leu Gly Ser Leu Asn Ser Pro Pro Thr Cys
        515   520   525

Val Leu Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys
    530   535   540

Ala Glu Ile Thr Ile Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys
545   550   555   560

Pro Val Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Thr Gly Leu
            565   570   575

Ser Gly Lys Glu Val Gln Trp Lys Met Tyr Glu Val Thr Asn Pro Lys
        580   585   590

Pro Lys Ser Val Ser Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala
        595   600   605

Val Gln Val Arg Phe Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn
    610   615   620

Trp Ser Asn Pro Ala Tyr Thr Val Val Met Asp Ile Lys Val Pro Met
625   630   635   640

Arg Gly Pro Glu Phe Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys
            645   650   655

Glu Lys Asn Val Tyr Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser
            660   665   670

8

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Leu Cys Ser Val Gln Arg Tyr Val Ile Asn His His Thr Ser Xaa Asn
        675                 680                 685

Gly Thr Trp Ser Glu Asn Val Gly Asn His Thr Lys Phe Thr Phe Leu
    690                 695                 700

Trp Thr Glu Gln Ala His Thr Val Thr Val Leu Ala Ile Asn Ser Ile
705             710                 715                 720

Gly Ala Ser Val Ala Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser
            725                 730                 735

Lys Val Asn Ile Val Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser
        740                 745                 750

Cys Val Ile Val Ser Trp Ile Leu Ser Pro Ser Asp Val Lys Leu Met
        755                 760                 765

Tyr Pro Ile Ile Glu Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys
    770                 775                 780

Trp Leu Arg Ile Ser Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His
785                 790                 795                 800

Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met
            805                 810                 815

Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Ser Phe Thr Gln Asn Asn
            820                 825                 830

Ile Glu Lys His Gln Ser Asp Ala Gly Leu Tyr Val Ile Val Pro Val
        835                 840                 845

Ile Ile Ser Ser Ser Ile Leu Leu Leu Gly Thr Leu Leu Ile Ser His
    850                 855                 860

Gln Arg Met Lys Lys Leu Phe Trp Glu Asp Val Pro Asn Pro Lys Asn
865                 870                 875                 880

Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Arg Thr Asn Ile Leu
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Leu Leu Met Leu Pro His Leu Gly Leu Gly Ala Ser Ile Ser
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<400> 17
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<210> 18
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<210> 19
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<210> 20
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tgattggtaa gaaaca                                                    16


<210> 21
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<400> 21
attgaggtat catagg                                                    16


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<210> 27
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<210> 28
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<210> 33

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<220>
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<400> 36
aaatttctag tgaagc                                              16


<210> 37
<211> 16
<212> DNA
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<220>
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<400> 37
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<210> 39
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<400> 43
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<220>
<221> UNSURE
<222> (31)
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            20   25   30

Thr Tyr Asp
        35